sequences had been reveresed is evident in examination of the related applications USSN 08/907,226 and USSN 08/129,112, on page 32, lines 2 and 3, which are incorporated by reference on page 1, lines 5-6 of the instant application.

The amendment to the paragraph beginning on page 13 line 9 corrects an inadvertent error in the assignment of SEQ ID NOS:4 and 5 to the degenerate PCR primers, since these assigned identifiers were already assigned previously (see page 5, lines 18-24).

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-14, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification and Claims by the current Amendment. The attached pages are captioned **"VERSION WITH MARKINGS TO SHOW CHANGES MADE."** As a convenience to the Examiner, a complete set of the Claims, as amended herein, is also attached to this Amendment as an Appendix entitled **"PENDING CLAIMS WITH ENTRY OF THE AMENDMENT."**

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 32 of page 2 has been amended as follows:

The present invention provides methods of modulating mycorhizal infection in a plants. The method comprise introducing into the plant an expression cassette containing a plant promoter operably linked to a heterologous LNP polynucleotide or complement thereof, wherein the LNP polynucleotide encodes an LNP polypeptide at least about 70% identical to SEQ ID NO:2, SEQ ID NO:4 ~~SEQ ID NO: 4~~, or SEQ ID NO:10 ~~SEQ ID NO: 6~~. The heterologous LNP polynucleotide can be SEQ ID NO:1. SEQ ID NO:3 ~~SEQ ID NO: 3~~, or SEQ ID NO:8 ~~SEQ ID NO: 5~~.

Paragraph beginning at line 18 of page 5 has been amended as follows:

An "LNP polynucleotide" is a nucleic acid sequence comprising (or consisting of) a coding region of about 100 to about 2000 nucleotides, sometimes from about 1400 to about 1500 nucleotides, which specifically hybridizes, to the *Dolichos biflorus* polynucleotide (SEQ ID NO:1), or to the *Lotus japonicus* polynucleotide (SEQ ID NO:8) ~~(SEQ ID NO:3)~~, or to the *Medicago sativa* polynucleotide (SEQ ID NO:3) ~~(SEQ ID NO:5)~~, or which encodes an LNP polypeptide. The isolation and characterization of the *Lotus* and *Medicago* genes are described in the PCT application WO 98/16261.

Paragraph beginning at line 25 of page 5 has been amended as follows:

An LNP polypeptide of the present invention comprises at least 50 amino acids, more preferably at least 100 amino acids, still more preferably at least 200 amino acids and most preferably up to about 500 amino acids from SEQ ID NO:2, SEQ ID NO:4, and SEQ ID NO:10 ~~SEQ ID NO:6~~, and conservatively modified varients thereof. The LNP polypeptides of the present invention also include proteins which have substantial identity to an LNP protein of at least 10 to 500 amino acids selected from SEQ ID NO:2, SEQ ID NO:4, and SEQ ID NO:10 ~~SEQ ID NO:6~~ and conservatively modified variants thereof.

Paragraph beginning at line 9 of page 11 has been amended as follows:

In the present invention, genomic DNA or cDNA comprising LNP nucleic acids of the invention can be identified in standard Southern blots under stringent conditions using the nucleic acid sequences disclosed here. For the purposes of this disclosure, suitable stringent conditions for such hybridizations are those which include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C ~~37 C~~, and at least one wash in 0.2X SSC at a temperature of at least about 50°C, usually about 55°C to about 60°C, for 20 minutes, or equivalent conditions. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

Paragraph beginning at line 9 of page 13 has been amended as follows:

Appropriate primers and probes for identifying LNP genes from Dolichos biflorus or transgenic plant tissues are generated from comparisons of the sequences provided herein. For a general overview of PCR see PCR PROTOCOLS: A GUIDE TO

METHODS AND APPLICATIONS, (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Appropriate degenerate primers for this invention include, for instance: a 5' PCR primer [5'-TA(T/C)GCNGTNAT(T/C)TT(T/C)GATGC-3'] (SEQ ID NO:13) ~~(SEQ ID NO:4)~~ and a 3' PCR primer [5'-AT(A/G)TT(A/G)TA(T/A/G)AT(G/A)CCNGG-3'] (SEQ ID NO:14) ~~(SEQ ID NO:5)~~ where N denotes all nucleotides. The amplification conditions are typically as follows. Reaction components: 10 mM Tris-HCl, pH 8.3, 50 mM potassium chloride, 1.5 mM magnesium chloride, 0.001% gelatin, 200 μM dATP, 200 μM dCTP, 200 μM dGTP, 200 μM dTTP, 0.4 μM primers, and 100 units per mL Taq polymerase. Program: 96°C for 3 min., 30 cycles of 96°C for 45 sec., 50°C for 60 sec., 72°C for 60 sec, followed by 72°C for 5 min.

Paragraph beginning at line 25 of page 13 has been amended as follows:

A preferred method is RACE (Frohman, et. al., *Proc. Nat'l. Acad. Sci. USA* 85:8998 (1988)). Briefly, this technique involves using PCR to amplify a DNA sequence using a random 5' primer and a defined 3' primer, e.g., ~~(SEQ ID NO:6)~~ (5' RACE) or a random 3' primer and a defined 5' primer, e.g., ~~(SEQ ID NO:7)~~ (3' RACE). The amplified sequence is then subcloned into a vector where it is then sequenced using standard techniques. Kits to perform RACE are commercially available (e.g. 5' RACE System, GIBCO BRL, Grand Island, New York, USA). In this manner, the entire LNP coding sequence of about 1600 bp can be obtained (SEQ ID NO:1). The invention also provides genomic sequence of the LNP (SEQ ID NO:3).

In the Claims:

Claims 1, 4 and 8 have been amended as follows:

1. (Amended) A method of modulating mycorhizal infection in a plant, the method comprising introducing into the plant an expression cassette containing a plant promoter operably linked to a heterologous *LNP* polynucleotide or complement thereof, wherein the *LNP* polynucleotide encodes an LNP polypeptide at least about 70% identical to SEQ ID NO:2, SEQ ID NO:4 ~~SEQ ID NO: 4~~, or SEQ ID NO:10. ~~SEQ ID NO: 6~~

4. (Amended) The method of claim 1, wherein the heterologous LNP polynucleotide is SEQ ID NO:8 ~~SEQ ID NO: 5~~.

8. (Amended) The method of claim 1, wherein the NBP46 polypeptide has an amino acid sequence as shown in SEQ ID NO:10 ~~SEQ ID NO: 6~~.

PENDING CLAIMS WITH ENTRY OF THE AMENDMENT

1. (Amended) A method of modulating mycorhizal infection in a plant, the method comprising introducing into the plant an expression cassette containing a plant promoter operably linked to a heterologous LNP polynucleotide or complement thereof, wherein the LNP polynucleotide encodes an LNP polypeptide at least about 70% identical to SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:10.

2. (As filed) The method of claim 1, wherein the heterologous LNP polynucleotide is SEQ ID NO:1.

3. (As filed) The method of claim 1, wherein the heterologous LNP polynucleotide is SEQ ID NO: 3.

4. (Amended) The method of claim 1, wherein the heterologous LNP polynucleotide is SEQ ID NO:8.

5. (As filed) The method of claim 1, wherein the plant promoter is from an LNP gene.

6. (As filed) The method of claim 1, wherein the NBP46 polypeptide has an amino acid sequence as shown in SEQ ID NO:2.

7. (As filed) The method of claim 1, wherein the NBP46 polypeptide has an amino acid sequence as shown in SEQ ID NO: 4.

8. (Amended) The method of claim 1, wherein the NBP46 polypeptide has an amino acid sequence as shown in SEQ ID NO:10.

9. (As filed) The method of claim 1, wherein the expression cassette is introduced into the plant through a sexual cross.

10. (As filed) The method of claim 1, wherein the promoter is linked to the *LNP* polynucleotide in an antisense orientation.

11. (As filed) The method of claim 1, wherein the promoter is linked to the *LNP* polynucleotide in a sense orientation.

12. (As filed) The method of claim 1, wherein expression of the *LNP* polynucleotide is enhanced, thereby increasing infection of the plant by a mycorrhizal fungus.

13. (As filed) The method of claim 1, further comprises infecting the plant with a mycorrhizal fungus.

14. (As filed) The method of claim 13, wherein the mycorrhizal fungus is *Glomus intraradices*.